

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2002, 17:40:41 ; Search time 20.26 Seconds

(without alignments)  
403.249 Million cell updates/sec

Title: US-09-502-984B-6

Perfect score: 1098

Sequence: 1 KFESKALLAARCPEDLCF.....AEPSFGFWMSAMSEPVSLLT 211

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1060	96.5	508	1	EPOR_HUMAN
2	877.5	79.9	507	1	EPOR_RAT
3	869.5	79.2	507	1	EPOR_MOUSE
4	171	15.6	625	1	TPOR_MOUSE
5	146	13.3	635	1	TPOR_HUMAN
6	118	10.7	581	1	PRUR_BOVIN
7	112.5	10.2	634	1	PRUR_BOVIN
8	111	10.1	522	1	IL9R_HUMAN
9	110.5	10.1	634	1	GHR_SHEEP
10	108	9.8	581	1	PRLR_CEREL
11	107	9.7	608	1	GHR_CHICK
12	104.5	9.5	611	1	GHR_COLLI
13	104	9.5	616	1	PRUR_RABIT
14	103.5	9.4	650	1	GHR_MOUSE
15	103.5	9.4	631	1	PRLR_CHICK
16	103	9.4	638	1	GHR_PIG
17	99.5	9.1	638	1	GHR_RABIT
18	99	9.0	831	1	PRUR_MEIGA
19	98.5	9.0	830	1	PRUR_COLLI
20	98	8.9	897	1	CYRB_HUMAN
21	96.5	8.8	378	1	IL3R_HUMAN
22	96	8.7	1165	1	LEPR_HUMAN
23	94	8.6	468	1	IL9R_MOUSE
24	92.5	8.4	638	1	GHR_RAT
25	92	8.4	2594	1	7LES_DROVI
26	91	8.3	608	1	PRUR_MOUSE
27	89	8.1	638	1	GHR_MACMU
28	88	8.0	622	1	PRUR_HUMAN
29	87	7.9	610	1	PRUR_RAT
30	85.5	7.8	863	1	AMPN_CAUCR
31	85	7.7	184	1	MPL_MPLV
32	84	7.7	336	1	CD11_MOUSE
33	84	7.7	485	1	HXKB_YEAST

## ALIGNMENTS

RESULT ID	1	EPOR_HUMAN	STANDARD:	PRT:	508 AA.
AC	P19235;				
DT	01-NOV-1990 (Rel. 16, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-MAR-2002 (Rel. 41, Last annotation update)				
DE	Erythropoietin receptor precursor (EPO-R).				
OS	EPOR.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-91372359; PubMed-1654273;				
RA	Ehrenman K., St John T.;				
RT	"The erythropoietin receptor gene: cloning and identification of				
RT	multiple transcripts in an erythroid cell line OCIM1.";				
RT	Exp. Hematol. 19:973-977(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-90304340; PubMed-2163696;				
RT	Jones S.S., D'Andrea A., Haines L.L., Wong G.G.;				
RT	"Human erythropoietin receptor: cloning, expression, and biologic				
RT	characterization.";				
RT	Blood 76:31-35(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE-92399733; PubMed-1668606;				
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,				
RA	Hankins W.D.;				
RT	"Cloning of the human erythropoietin receptor gene.";				
RT	Blood 78:2548-2556(1991).				
RN	[4]				
RP	SEQUENCE OF 1-96 FROM N.A.				
RC	TISSUE=Placenta;				
RX	MEDLINE-92399734; PubMed-1668607;				
RA	Maouche L., Tournamille C., Hattab C., Boffa G., Cartton J.P.,				
RA	Chretien S.;				
RT	"Cloning of the gene encoding the human erythropoietin receptor.";				
RT	Blood 78:2557-2563(1991).				
RN	[5]				
RP	SEQUENCE OF 1-17 FROM N.A.				
RX	MEDLINE-92147143; PubMed-1664413;				
RA	Penny L.A., Forget B.G.;				
RT	"Genomic organization of the human erythropoietin receptor gene.";				
RT	Genomics 11:974-980(1991).				
RN	[6]				
RP	X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 34-244.				
RX	MEDLINE-96291992; PubMed-8662530;				
RA	Livnah O., Stura E.A., Johnson D.L., Middleton S.A., Mulachy L.S.,				
RA	Wrighton N.C., Dower W.J., Jolliffe L.K., Wilson I.A.;				
RT	"Functional mimicry of a protein hormone by a peptide agonist: the				
RT	EPO receptor complex at 2.8 A.";				

```

RL Science 273:464-471(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 34-244.
RX MEDLINE=99023198; PubMed=9808045;
RA Livneh O., Johnson D.L., Stura E.A., Farrell F.X., Barbone F.P.,
RA Jolliffe L.K., Wilson I.A.;
RA You Y., Liu K.D., Goldsmith M.A., He W., Krause C.D., Festha S.,
RA "An antagonist peptide-EPO receptor complex suggests that receptor
RT dimerization is not sufficient for activation.";
RL Nat. Struct. Biol. 5:993-1004(1998).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 32-244 IN COMPLEX WITH EPO.
RX MEDLINE=98445092; PubMed=9774108;
RA Syed R.S., Reid S.W., Li C., Cheatham J.C., Aoki K.H., Liu B.,
RA Zhan H., Osslund T.D., Chirino A.J., Zhang J., Finer-Moore J.,
RA Elliott S., Stoney K., Katz B.A., Matthews D.J., Wendoloski J.J.,
RA Egrie J., Stroud R.M.;
RT "Efficiency of signalling through cytokine receptors depends
RT critically on receptor orientation.";
RL Nature 395:511-516(1998).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M34986; AA52401.1; -
DR EMBL: M60459; AA52403.1; -
DR EMBL: S45352; AA82371.1; -
DR EMBL: M76595; AA52393.1; -
DR EMBL: M77244; AA52392.1; -
DR PIR: A43799; A43799.
DR PIR: A49824; A49824.
DR PIR: A53958; A53958.
DR PDB: 1EBP; 29-JUL-97.
DR PDB: 1EBA; 18-NOV-98.
DR PDB: 1EER; 01-OCT-99.
DR PDB: 1CN4; 11-AUG-99.
DR MIM: 133171; -
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; Hematopo_REC_L_F1; 1.
KM Receptor; Transmembrane; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 508
FT DOMAIN 25 250 ERYTHROPOIETIN RECEPTOR.
FT TRANSMEM 251 273 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 274 508 POTENTIAL.
FT DOMAIN 148 213 CYTOPLASMIC (POTENTIAL).
FT DISULFID 52 62 FIBRONECTIN TYPE-III.
FT DISULFID 91 107
FT CARBOHYD 76 76
SQ SEQUENCE 508 AA; 55065 MW; F9F326E162E9512A CRC64;
N-LINKED (GLCNAC....) (POTENTIAL).
Query Match 96.5%; Score 1060; DB 1; Length 508;
Best Local Similarity 93.8%; Pred. No. 5.7e-96;
Matches 198; Conservative 11; Mismatches 2; Indels 0; Gaps 0;
1 KESKAALLAARGPEELCTERIEDLVCFEEAASAGVPGNFSFQLEDEPWKICRL 60
|||||

```

```

DB 34 KESKAALLAARGPEELCTERIEDLVCFEEAASAGVPGNFSFQLEDEPWKICRL 93
QY 61 HQAPTANGAIRFWCSLTPTADTSSFPLERLTLTAAGAPRRHVIHNEVLLDAPVGLVA 120
DB 94 HQAPTANGAIRFWCSLTPTADTSSFPLERLTLTAAGAPRRHVIHNEVLLDAPVGLVA 153
QY 121 RLADSGHVIVIRLPPETPMTSIRFELDISAGNGAGSVQVRELLGRTCEVLSNIGR 180
DB 154 RLADSGHVIVIRLPPETPMTSIRFELDISAGNGAGSVQVRELLGRTCEVLSNIGR 213
QY 181 TRITIAVRARMAEPSPGFGWSAMSEPVSLT 211
DB 214 TRYFAVRARMAEPSPGFGWSAMSEPVSLT 244
RESULT 2
EPOR_RAT
ID EPOR_RAT STANDARD; PRT; 507 AA.
AC Q07303;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Erythropoietin receptor precursor (EPO-R).
GN EPOR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9326574; PubMed=7684373;
RA Masuda S., Nagao M., Takahata K., Konishi Y., Gallys F.,
RA Tabita T., Sasaki R.;
RT "Functional erythropoietin receptor of the cells with neural
RT characteristics. Comparison with receptor properties of erythroid
RT cells.";
RL J. Biol. Chem. 268:11208-11216(1993).
CC -1- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC AND DIFFERENTIATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D13566; BAA02761.1; -
DR PIR: A46713; A46713.
DR HSP: P19235; 1EBA.
DR InterPro: IPR002996; CR1A.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003528; Hematopo_receptor_L_F1.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
DR PROSITE: PS01352; Hematopo_REC_L_F1; 1.
KM Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 507
FT DOMAIN 25 249 ERYTHROPOIETIN RECEPTOR.
FT TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 273 507 POTENTIAL.
FT DOMAIN 147 212 CYTOPLASMIC (POTENTIAL).
FT DISULFID 52 62 FIBRONECTIN TYPE-III.
FT DISULFID 90 106
FT CARBOHYD 75 75
SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64;
N-LINKED (GLCNAC....) (POTENTIAL).

```

	Query Match Similarity	79.9%	Score 877.5;	DB 1;	Length 507;
	Best Local Similarity	78.2%	Pred. No. 3.8e-78;		
	Matches 165; Conservative	23;	Mismatches 22;	Indels 1;	Gaps 1.
OY	1	KFEESKAALLAARGPELLCFTERLEDLYCFEEBAASAGVPGNFSFQLEDEPMKICRL	60		
Dd	34	KFEESKAALLASGSELLCFTORLEDLYCFEEMANSCMG - PNYSPSYOJEGESRKRSL	92		
OY	61	HOAPFAACAIRPWCGLPADTSSFPYLELR.LTAAGCAPGFHVHINHEVLLDADPGLVA	120		
Dd	93	HOAPFVKSMRWCSLPADTSSFPYLEQTVLEAGSGSPRYARI IHNEVLLDADPGLLA	152		
OY	121	FLADESGHVIVIRLPPETPMTSATIRFELDLSAGACGAGSVQVELLEGRETCVLSTNLGR	180		
Dd	153	RRAEGSHVILRLMDPPGPMTTHIRIYEVDASGNRAGGTQAVEVLEGTCEVLSTNLRG	212		
OY	181	TRITIAVARARAAEPSEFGFMASMEPSVSLTT	211		
Dd	213	TRYTFVARARAAEPSFGFMASMEPSASLT	243		

ID	EPOR_MOUSE	STANDARD:	PRT:	507 AA.
AC	P14753; 063852;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Erythropoietin receptor precursor (EPO-R).			
CN	EPOR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89195238; Pubmed=2539263;			
RA	D'Andrea A.D., Lodish H.F., Wong G.G.;			
RT	"Expression cloning of the murine erythropoietin receptor.";			
RL	Cell 57:277-285(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BALB/C; TISSUE=Liver;			
RX	MEDLINE=91080149; Pubmed=2175360;			
RA	Kuramochi S., Ikawa Y., Todokoro K.;			
RT	"Characterization of murine erythropoietin receptor genes.";			
RL	J. Mol. Biol. 216:567-575(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92017832; Pubmed=1656233;			
RA	Hino M., Tojo A., Misawa Y., Morii H., Takaku F., Shbuya M.;			
RT	"Unregulated expression of the erythropoietin receptor gene caused by			
RT	insertion of spleen focus-forming virus long terminal repeat in a			
RL	murine erythroleukemia cell line.";			
RL	Mol. Cell. Biol. 11:5527-5533(1991).			
RN	[4]			
RP	SEQUENCE OF 1-27 FROM N.A.			
RX	MEDLINE=90287158; Pubmed=2162479;			
RA	Yousoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;			
RT	"Structure and transcription of the mouse erythropoietin receptor			
RT	gene.";			
RL	Mol. Cell. Biol. 10:3675-3682(1990).			
RN	[5]			
RP	SEQUENCE OF 1-24 FROM N.A.			
RX	MEDLINE=91201346; Pubmed=1849897;			
RA	Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H.;			
RA	Gisselbrecht S., Cartton J.P.;			
RT	"Spleen focus-forming virus long terminal repeat insertional			
RT	activation of the murine erythropoietin receptor gene in the T3C1-2			
RT	friend leukemia cell line.";			
RL	J. Biol. Chem. 266:6952-6956(1991).			
RN	[6]			

RP	MUTAGENESIS.
RX	MEDLINE:93180826; PubMed=8382775;
RA	Mura O., Cleveland J.L., Ihle J.N.;
RT	"Inactivation of erythropoietin receptor function by point mutations
RT	in a region having homology with other cytokine receptors.";
RL	Mol. Cell. Biol. 13:1788-1795(1993).
CC	- FUNCTION: RECEPTOR FOR ERYTHROPOIETIN. MAY PLAY A ROLE IN THE
CC	MECHANISM OF ERYTHROPOIETIN-INDUCED ERYTHROBLAST PROLIFERATION
CC	AND DIFFERENTIATION.
CC	- SUBCELLULAR LOCATION: Type I membrane protein.
CC	- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC	- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; J04843; AAA37571.1; -
DR	EMBL; X53081; CA937248.1; -
DR	EMBL; M38133; AAA37572.1; -
DR	EMBL; M62360; AAA37582.1; -
DR	EMBL; S59388; AAB20029.2; -
DR	PIR; A32385; A32385.
DR	PIR; A41686; A41686.
DR	PIR; S13249; S13249.
DR	PIR; S14081; S14081.
DR	HSSP; P19235; 1EBA.
DR	MCD; MGI:95408; Epor.
DR	InterPro: IPR002996; CRIA.
DR	InterPro: IPR003961; FN.III.
DR	InterPro: IPR003528; Hematopo_receptor_L.F1.
DR	Pfam; PF00041; fn3; 1.
DR	SMART; SM00060; FN3; 1.
DR	PROSITE; PS01352; HEMATOPO_REC_L.F1; 1.
KW	Receptor; Transmembrane; Glycoprotein; signal.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DISULFID
FT	DISULFID
FT	CARBOHD
FT	CONFLICT
SO	SEQUENCE
	507 AA; 55194 MW; 067657A2E26451CA CRC64;
	E -> D (IN REF. 3; AAB20029).
	N-LINKED (GLCNAC, ...) (POTENTIAL).
	ERYTHROPOIETIN RECEPTOR.
	EXTRACELLULAR (POTENTIAL).
	POTENTIAL.
	CYTOPLASMIC (POTENTIAL).
	FIBRONECTIN TYPE-III.
	BY SIMILARITY.
	BY SIMILARITY.
	BY SIMILARITY.

[illegible]

ID	TPOR_MOUSE	STANDARD:	PRT:	625 AA.
TPOR_MOUSE	TPOR_MOUSE			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Thrombopoietin receptor precursor (PRO-R) (Myeloproliferative leukemia protein) (C-mpl).			
DE	MPL OR TPOR.			
GN	MPL OR TPOR.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10990;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RX	MEDLINE=93327753; PubMed=8334987;			
RA	Skoda R.C., Seldin D.C., Chiang M.K., Peichel C.L., Vogt T.F.,			
RA	Leder P.;			
RT	"Murine c-mpl: a member of the hematopoietic growth factor receptor			
RT	superfamily that transduces a proliferative signal.";			
RL	EMBL J. 12:2645-2653(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=ICFW; TISSUE=Fetal liver;			
RX	MEDLINE=93390934; PubMed=8397366;			
RA	Vignon I., Florindo C., Fichelson S., Guenet J.-L., Mattel M.-G.,			
RA	Souyri M., Cosman D., Gisselbrecht S.;			
RT	"Characterization of the murine Mpl proto-oncogene, a member of the			
RT	hematopoietic cytokine receptor family: molecular cloning,			
RT	chromosomal location and evidence for a function in cell growth.";			
RL	Oncogene 8:2607-2615(1993).			
CC	-1- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY			
CC	MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).			
CC	-----			
DR	EMBL: Z22649; CA80365.1; -;			
DR	EMBL: Z22657; CA80372.1; -;			
DR	EMBL: X73677; CA852031.1; -;			
DR	PIR: S35317; S35317.			
DR	HSSP: P19235; IEBA.			
DR	MCD: MGI:97076; Mpl.			
DR	InterPro: IPR002996; CRIA.			
DR	InterPro: IPR003961; FN_III.			
DR	InterPro: IPR003528; Hematopo_receptor_L_F1.			
DR	Planm; PF00041; In3; 1.			
DR	SMART; SMO0060; FN3; 1.			
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.			
KW	Receptor; Transmembrane; Glycoprotein; Signal; Repeat.			
FT	SIGNAL	1	25	POTENTIAL.
FT	CHAIN	26	625	THROMBOPOIETIN RECEPTOR.
FT	DOMAIN	26	482	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	483	504	POTENTIAL.
FT	DOMAIN	505	625	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	117	117	N-LINKED (GLCNAc. . .) (POTENTIAL).
FT	CONFLICT	2	8	MISSING (IN REF. 2).
FT	CONFLICT	99	99	D -> V (IN REF. 2).
FT	CONFLICT	222	222	P -> PNTSPAGE (IN REF. 2).
SO	SEQUENCE	625 AA;	69817 MW;	309CFEEAA3724549 CRC64;

```

Matches 62: Conservative 33: Mismatches 105: Indels 52: Gaps 8
QY 4 SKAALLANGPELLCTFERLEDLYCFEEFASAGVGNPFSEFQLEDEPMKICRLHQA 63
Db 25 SDVFLLAAGTPELNCESQTFEDLFCFMEEDBA--PSGTQLLVAYRGEKPRACPYSQ 82
QY 64 PARGAFRCWCSLPPAD-TSSFVPLERLTAAS-GAPRRYIHINEVLLDAPGVLYAR 121
Db 83 SVPTGTRVCCFPADQVRLFFPLHLWKNVNSLNOTLQIRLPLVDVSLPAPRYIKAR 142
QY 122 IADSGHVIVRN-LPPETPMTSHIRFELDI---SAGNAGSVORVELLEGRT----- 170
Db 143 GSGQGEGLQIHMEADAPE--ISDFLRHRLRYGPTDSSNATAESV--IQLLSTETCCPLLM 198
QY 171 -----ECVLSLRGRTRTTIVARRMAEPSCG 197
Db 199 MNPVPVLDPPCVHPTASQPHGAPFLRVKGGSCGLVSGLQASKSYMLQIRSQPDGVSLR 258
QY 198 GFWSAMSEPVSL 209
Db 259 GSWGPMSEPVTV 270

RESULT 5
TPOR_HUMAN
ID TPOR_HUMAN STANDARD: PRT: 635 AA.
AC P40238;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Thrombopoietin receptor precursor (PRO-R) (Myeloproliferative leukemia
DE protein) (C-MPL) (CD110 antigen).
GN MPL OR TPOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92302297; PubMed=1608974;
RA Vigon I., Morron J.-P., Coccault L., Mitjavila M.-T., Tambourin P.,
RA Giesbrecht S., Souyri M.;
RT "Molecular cloning and characterization of MPL, the human homolog of
RT the v-mpl oncogene: Identification of a member of the hematopoietic
RT growth factor receptor superfamily."
RL Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94292186; PubMed=8020956;
RA Migotte V., Vigon I., de Crevecoeur E., Romeo P.H., Lemarchandel V.,
RA Chretien S.;
RT "Structure and transcription of the human c-mpl gene (MPL).";
RL Genomics 20:5-12(1994).
CC -I- FUNCTION: RECEPTOR FOR THROMBOPOIETIN. MAY REPRESENT A REGULATORY
CC MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMUNE RESPONSES.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: C-MPL-K (SHOWN HERE) AND C-MPL-
CC P; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -I- TISSUE SPECIFICITY: EXPRESSED AT A LOW LEVEL IN A LARGE NUMBER OF
CC CELLS OF HEMATOPOIETIC ORIGIN. THE TWO FORMS (C-MPL-K AND C-MPL-
CC P) ARE ALWAYS FOUND TO BE COEXPRESSED.
CC -I- DISEASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC
CC THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATED
CC THROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO PHYSICAL
CC ANOMALIES.
CC -I- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -I- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -I- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-8 IS THE INITIATOR.
CC -I- DATABASE: NAME=PROW; NOTE=cd guide CD110 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/1158625.g.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```





```

DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003531; Hematopo_receptor_S_F1.
DR PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 40
FT CHAIN 1 522
FT DOMAIN 41 522 INTERLEUKIN-9 RECEPTOR.
FT TRANSMEM 271 291 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 292 522 POTENTIAL.
FT DOMAIN 150 244 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 429 439 FIBRONECTIN TYPE-III.
FT DOMAIN 440 443 POLY-SER.
FT CARBOHYD 117 117 POLY-ASN.
FT CARBOHYD 156 156 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 439 439 R -> G (IN REF. 3).
FT CONFLICT 439 439 MISSING (IN REF. 3).
SQ SEQUENCE 522 AA; 57333 MW; E6CB5C6342DEB2 CRC64;

Query Match 10.1%; Score 111; DB 1; Length 522;
Best Local Similarity 23.7%; Pred. No. 0.0029;
Matches 53; Conservative 28; Mismatches 97; Indels 46; Gaps 11;

OY 12 RGPBE--LLCTFERLEDLYCFEEAASAGVGPNGFSFQLEDEPWKLCRLHQAPTARGA 69
DB 47 QGPRSRTEFTCLTNILNRIDCHW-SAPELGQG-----SSPWLLFTSNQAPGCTHK 94
OY 70 IRFMCSLPTADSSFPLELRITLTAAG-APRHRYHINEV-----VLLDAP 115
DB 95 ----CILKSGSECTVLPPEAVLVPSDNTITTFHHCMSGREQVSLVDPEYLPRRHVKLDP 150
OY 116 VGLVRLADESGHVVIRW-LPPETPMTHSHIRFELDISANGCA-GSVGRVELLEGTECV 173
DB 151 SLOQSNIS--SCHCLTMSISPALERPMTLLSYELAFKQGEAQAQRDHIVGTWLI 208
OY 174 LSNL-----RGRRTITAVRAR-MAEPSFGGFWASMEPV 207
DB 209 LEAFELDPGFIEARLRVQMATLEDDVVEERYTGQWSEMSQPV 252

RESULT 9
GHR_SHEEP STANDARD: PRT; 634 AA.
AC Q28575;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
DE GHR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91099608; PubMed=1980117;
RA Adams T.E., Baker L., Fildes R.J., Brandon M.R.;
RT "The sheep growth hormone receptor: molecular cloning and ontogeny of
RT mRNA expression in the liver."
RL Mol. Cell. Endocrinol. 73:135-145(1990).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M82912; AA73171.1; -.
DR HSSP; P10912; IAXI.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hematopo_receptor_L_F1.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
KW PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 18
FT CHAIN 1 19
FT DOMAIN 19 260 GROWTH HORMONE RECEPTOR.
FT TRANSMEM 261 284 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 285 634 POTENTIAL.
FT DOMAIN 141 248 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 108 FIBRONECTIN TYPE-III.
FT DISULFID 122 136 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 196 196 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 634 AA; 70844 MW; FFD28B9C23EC1496 CRC64;

Query Match 10.1%; Score 110.5; DB 1; Length 634;
Best Local Similarity 26.6%; Pred. No. 0.0041;
Matches 34; Conservative 24; Mismatches 57; Indels 13; Gaps 5;

OY 19 CETERLEDLYCFEEAASAGV-GPGNFS-FSQLEDEPWKLCRLHQAPTARGAIRFWSL 76
DB 56 CSPELETFSCWMTDQANHSIQSPSVQMFIRRDIOEKEC-----PDYVAGENSQYF 110
OY 77 PTADTSSFPLELRITLTAAGAPRHRYHINEVLLDAPVGLVARLADS-----GHVVI 131
DB 111 NSSYSTSWTPYCIKILTSNGIVD-HKCFSEVEDIVOPDPVGLMTWLITSLREIHADILV 169
OY 132 RWLPPPET 139
DB 170 KWPEPPPT 177

RESULT 10
PRLR_CEREL STANDARD: PRT; 581 AA.
AC Q28235;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
DE PRLR.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96030711; PubMed=7561644;
RA Clarke L.A., Edey M., London A.S., Randall V.A., Postel-Vinay M.C.,
RA Kelly P.A., Jabbour H.N.;
RT "Expression of the prolactin receptor gene during the breeding and
RT non-breeding seasons in red deer (Cervus elaphus): evidence for the
RT expression of two forms in the testis."
RL J. Endocrinol. 146:313-321(1995).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

```



```

CC PROLACTIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X39933; CAA64419.1; -.
CC HSSP: P14787; IAN3.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003961; FN.III.
CC InterPro: IPR003528; Hematopo_receptor_L_F1.
CC Pfam: PF00041; fn3; 2.
CC SMART: SM00060; fn3; 1.
CC PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
CC FT SIGNAL 1 24
CC FT CHAIN 25 581
CC FT DOMAIN 25 234
CC FT TRANSMEM 235 258
CC FT DOMAIN 259 581
CC FT DOMAIN 25 122
CC FT DOMAIN 123 227
CC FT DISULFID 36 46
CC FT DISULFID 75 86
CC FT CARBOHYD 59 59
CC FT CARBOHYD 132 132
CC FT CARBOHYD 233 233
CC SEQUENCE 581 AA; 65159 MW; 975E47CB63CF28EC CRC64;

Query Match 9.8%; Score 108; DB 1; Length 581;
Best Local Similarity 20.7%; Pred. No. 0.0064;
Matches 43; Conservative 41; Mismatches 98; Indels 26; Gaps 9;

QY 14 PELLCTERLELDVCFEEFAASAGVGNGFSPFOLEDEPWKICRLHOAPFARGAIFRW 73
DB 31 PKIKCRSPKKEFTFCWMEGSDGL-PTNYTLTYHKEGE-----TLIHEPDKTKGSPNT 85
QY 74 CSLPTADTSSFVLEELRLTA-----ASGAPRFRVTHINEVLLDAPVGLVARL--AD 124
DB 86 CYFSKRTSIWKIYVITVNAINQMGVSSDPLX---VDVYIYIEPPEPAMLTLELKHPE 142
QY 125 ESGHVYIRMLPPEPTPMTS---HIREFLDISAGNGAGSVORVELLEGRTECVLSNLGRGT 181
DB 143 RKPYLWKMPPTPLTDVKSQMFMYEIRLKPETAAD--WEIHFAAKOTOLKITSFVPGQ 200
QY 182 RITIAVARARMAEPSPFGFMSWSEPVS 209
DB 201 KYLVQVACK---PDH-CYMSSEMPSESI 224

RESULT 11
GHR_CHICK ID STANDARD; PRT; 608 AA.
AC 002092;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Growth hormone receptor precursor (GH receptor) (Serum binding
DE protein).
GN GHR.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;

```

```

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91243665; PubMed=2036984;
RA Burnside J, Liou S.S, Copburn L.A.;
RT "Molecular cloning of the chicken growth hormone receptor
RT complementary deoxyribonucleic acid: mutation of the gene in
RT sex-linked dwarf chickens.";
RL Endocrinology 128:3183-3192(1991).
CC -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: BROAD SPECIFICITY.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M74057; AAA48781.1; -.
CC PIR: S32823; S32823.
CC HSSP: P10912; IHW.
CC InterPro: IPR002996; CRIA.
CC InterPro: IPR003961; FN.III.
CC InterPro: IPR003528; Hematopo_receptor_L_F1.
CC Pfam: PF00041; fn3; 1.
CC SMART: SM00060; fn3; 1.
CC PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
CC Receptor; Transmembrane; Glycoprotein; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 608
CC FT DOMAIN 17 237
CC FT TRANSMEM 238 261
CC FT DOMAIN 262 608
CC FT DOMAIN 117 223
CC FT DOMAIN 34 44
CC FT DISULFID 72 83
CC FT DISULFID 97 111
CC FT CARBOHYD 86 86
CC FT CARBOHYD 127 127
CC FT CARBOHYD 132 132
CC FT CARBOHYD 171 171
CC SEQUENCE 608 AA; 68572 MW; D71AD7B6C62528DC CRC64;

Query Match 9.7%; Score 107; DB 1; Length 608;
Best Local Similarity 26.7%; Pred. No. 0.0085;
Matches 54; Conservative 26; Mismatches 90; Indels 32; Gaps 9;

QY 14 PELLCTERLELDVCFEEFAASAGVGNGFSPFOLEDEPWKICRLHOAPFARG 68
DB 29 PQISKCRSPLETFSCWTWD-----GKVTTSGLIQLLYKKRSDDEKEC-----PDYIT 77
QY 69 AIRFWCSLPTADTSSFVLEELRLTAASGAPRFRVTHINEVLLDAPVGLVARLADES-- 126
DB 78 AGNSCYFNSTSYTSIMPYVKL-ANKDEVFDEKCFSEVDIYLPDPVYHLMWTLMTSQ 136
QY 127 ---GHVYIRMLPPEPTPMTS---HIREFLDISAGNGAGSVORVELLEGRTECV--LSNR 178
DB 137 GIHGDIQVRWDPPEPFDVQGWITLLEYELQYKKEVNET---KKKELEPRLSTVVPYSLK 192
QY 179 GRTRTIAVARARMAEPSPFGF 199
DB 193 MGRDYELIRVRSRORTSEKGEF 214

RESULT 12
GHR_COLL

```



```

ID  GHR.COLLI          STANDARD;          PRT;          611 AA.
AC  Q90375;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  01-NOV-1997 (Rel. 35, Last annotation update)
DE  Growth hormone receptor precursor (GH receptor) (Serum binding
GN  protein).
OS  Columba livia (Domestic pigeon).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Columbiformes; Columbidae; Columba.
OX  NCBI_TaxID=8932;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Liver;
RA  Cheng C.H.K., Shaw P.C., Tsim K.W.K., Lau K.F.;
RL  Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
CC  -1- FUNCTION: THIS IS A RECEPTOR FOR PITUITARY GLAND GROWTH HORMONE.
CC  -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC  -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: U20353; AAA84745.1; -.
DR  HSSP: P10912; IAXI.
DR  InterPro: IPR002996; CRIA.
DR  InterPro: IPR003961; FN_III.
DR  InterPro: IPR003528; Hematopo_receptor_L_F1.
DR  Pfam: PF00041; fn3; 1.
DR  SMART: SM00060; FN3; 1.
DR  PROSITE: PS01352; Hematopo_REC_L_F1; 1.
KW  Receptor; Transmembrane; Glycoprotein; Signal.
FT  SIGNAL          1      20
FT  CHAIN           1      611
FT  DOMAIN          21     240
FT  TRANSMEM       241     264
FT  DOMAIN          265     611
FT  DOMAIN          119     226
FT  DISULFID        34      44
FT  DISULFID        75      86
FT  DISULFID        100     114
FT  CARBOHYD        16      16
FT  CARBOHYD        53      53
FT  CARBOHYD        89      89
FT  CARBOHYD        130     130
FT  CARBOHYD        135     135
FT  CARBOHYD        174     174
FT  CARBOHYD        174     174
FT  SEQUENCE        611 AA; 68851 MW; C48750BF9E4BDA CRC64;
SQ
Query Match          9.5%; Score 104.5; DB 1; Length 611;
Best Local Similarity 26.2%; Pred. No. 0.015;
Matches 53; Conservative 28; Mismatches 96; Indels 25; Gaps 10;

```

```

OY  179 GRTRITAVARM-AEPSEGF 199
    | 11:1 111
DB  196 IGRDYRVRVRSQRTSEKGEF 217

RESULT 13
PRLR_RABIT
ID  PRLR_RABIT          STANDARD;          PRT;          616 AA.
AC  P14787;
DT  01-APR-1990 (Rel. 14, Created)
DT  01-APR-1990 (Rel. 14, Last sequence update)
DT  15-JUL-1998 (Rel. 36, Last annotation update)
DE  Prolactin receptor precursor (PRL-R).
GN  PRLR.
OS  Oryctolagus cuniculus (Rabbit).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX  NCBI_TaxID=9986;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Mammary gland;
RX  MEDLINE=89184578; PubMed=2928321;
RA  Edey M., Jolicoeur C., Levi-Meyrueis C., Dusanter-Fourt I.,
RA  Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;
RT  "Identification and sequence analysis of a second form of prolactin
RT  receptor by molecular cloning of complementary DNA from rabbit
RT  mammary gland.";
RL  Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
RN  [2]
RP  3D-STRUCTURE MODELING OF 30-228.
RX  MEDLINE=97248733; PubMed=9094747;
RA  Halaby D., Thoreau E., Djiane J., Morron J.P.;
RT  "Homology modeling of rabbit prolactin hormone complexed with its
RT  receptor.";
RL  Proteins 27:459-468(1997).
CC  -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC  PROLACTIN.
CC  -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC  -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: J04510; AAA31457.1; -.
DR  PIR: A30304; A30304.
DR  PDB: 1AN3; 03-DEC-97.
DR  InterPro: IPR002996; CRIA.
DR  InterPro: IPR003961; FN_III.
DR  InterPro: IPR003528; Hematopo_receptor_L_F1.
DR  Pfam: PF00041; fn3; 2.
DR  SMART: SM00060; FN3; 2.
DR  PROSITE: PS01352; Hematopo_REC_L_F1; 1.
KW  Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
FT  SIGNAL          1      24
FT  CHAIN           1      616
FT  DOMAIN          25     234
FT  TRANSMEM       235     258
FT  DOMAIN          259     616
FT  DOMAIN          124     227
FT  DISULFID        36      46
FT  DISULFID        75      86
FT  CARBOHYD        59      59
FT  CARBOHYD        104     104
FT  CARBOHYD        132     132
FT  SEQUENCE        616 AA; 68840 MW; 800E3166FEF7108C CRC64;
SQ

```



FT VARSLIC 297 650 MISSING (IN ISOFORM 2).  
 FT CONFLICT 25 25 T -> A (IN REF. 6).  
 FT CONFLICT 162 162 G -> A (IN REF. 3 AND 4).  
 FT CONFLICT 325 325 E -> G (IN REF. 2).  
 FT CONFLICT 423 423 R -> A (IN REF. 2).  
 SQ SEQUENCE 650 AA; 72783 MW; 95653380CAF0B931 CRC64;

Query Match 9.4%; Score 103.5; DB 1; Length 650;  
 Best Local Similarity 22.6%; Pred. No. 0.02; Mismatches 39; Indels 47; Gaps 10;  
 Matches 51; Conservative 39;

QY 14 PERLLCFTEFLDVCFFEEAASAGV-GPGNFSFSDLED-----EPWKLGR 59  
 DB 51 PRRTKCRSPLELFSCYWMGNDPLKPGSIDLYAKRRSQARIAHEMTQENKEC- 109  
 QY 60 LHOAPFARGAIRFWCSLPTADTSSVPLELRTPAASGAPFRHVIHINEVLLDAPVGL 119  
 DB 110 ---PQVSAKNSCYENSYSITWIPYCIKLT-TMGDLIDQKCFVDEIVDPDPPIGLN 164  
 QY 120 ARLADS-----GHVYIRMLPPEPTF-MTSHIFELDISANGAGSVQVELLEGR---- 169  
 DB 165 WILNLSLGIKRGDIOVSWOPPNADVLKGMILEYET-----QYKVESKWKVM 215  
 QY 170 -----TECVLSNLRGRTITIAVARMAEPSEFGFSWAMSEPVSL 210  
 DB 216 GPWLTYCPYSLRMDKEHEVYRSR--QRFSEKY--SEFEVLRVI 258

RESULT 15  
 ID PRLR-CHICK STANDARD; PRT; 831 AA.  
 AC 004594;

DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Prolactin receptor precursor (PRL-R) (CPRLP).  
 GN PRLR.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosaurii; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-WHITE LEGHORN; TISSUE-Kidney;  
 RX MEDLINE-93075121; PubMed-1445292;

RA Tanaka M., Maeda K., Okubo T., Nakashima K.;  
 RT "Double antenna structure of chicken prolactin receptor deduced from  
 the cDNA sequence."  
 RL Biochem. Biophys. Res. Commun. 188:490-496(1992).  
 CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE  
 PROLACTIN

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation-  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))

DR EMBL: D13154; BA002439.1; -  
 DR PIR: J01655; J01655.  
 DR HSSP: P14787; IAN3.  
 DR InterPro: IPR002396; CRIA.  
 DR InterPro: IPR003961; FN\_III.  
 DR InterPro: IPR003528; Hematopo\_receptor\_L\_F1.  
 DR Pfam: PF00041; fn3; 4.  
 DR SMART: SM00060; FN3; 3.

DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; 1.  
 KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 23 POTENTIAL.  
 FT CHAIN 24 831 PROLACTIN RECEPTOR.  
 FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 439 459 POTENTIAL.  
 FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.  
 FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.  
 FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.  
 FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.  
 FT DISULFID 36 46 BY SIMILARITY.  
 FT CARBOHYD 59 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 335 335 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 831 AA; 94102 MW; 1CAE75791DCADB9 CRC64;

Query Match 9.4%; Score 103.5; DB 1; Length 831;  
 Best Local Similarity 20.0%; Pred. No. 0.027; Mismatches 102; Indels 29; Gaps 8;  
 Matches 42; Conservative 37;

QY 5 KAALLAARGPEELCFTEFLDVCFFEEAASAGVGPNGNFSFSDLEDPEFWKLCRLHOAP 64  
 DB 233 KPIILRCRSEK-----EFTCMWKPGLDGG-HPTNTLLYSNGEE--QYEECP 279  
 QY 65 TANGAIRFWCSLPTADTSSVPLELRTPA-----SGAPFRHVIHINEVLLDAPVGL 118  
 DB 280 DYTAPGPNSCYFDKKTSTFTIYNITVRATNENGSNSDPHY--VDVYIYQDPDPVNV 336  
 QY 119 VARL---ADESGHVYIRMLPPEPTMTS-HIRELDISANGAGSVQVELLEGRTECVL 174  
 DB 337 TLELKRPIKKPYLVLTWSPPLADYSGWLTLEYELRLKPERGEEMETTFVGQOTQYKM 396  
 QY 175 SNLRGRTITIAVARMAEPSEFGFSWAMSEPVSL 204  
 DB 397 FSLNPGKKYIIOIHK---PDHHSMSSEWS 423

Search completed: August 28, 2002, 17:40:42  
 Job time: 533 sec

---